

Kernel Quality Association and Path Analysis in Bread Wheat

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Abstract

The correlation and path coefficient analysis of some kernel quality traits have been studied for 92 cultivars, breeding lines and landrace varieties of bread wheat (*Triticum aestivum* L.). Ninety-two genotypes were evaluated in alpha lattice design with two replications. Result of analysis of variance indicated that there were significant differences among genotypes in the most of traits. The correlation analysis showed that there were significant positive correlations among thousand kernel weight (TKW), grain length (GL) and grain width (GW). We also showed TKW, GL and GW had positive correlation with grain protein percentage, gluten weight, and falling number. Grain protein was significantly correlated with several kernel characteristics including: TKW, GL, GW, hardness index, gluten weight, SDS sedimentation, and falling number. On the first and second steps of stepwise regression analysis, protein percentage and falling number were the most effective traits in explaining different trait variations. Path coefficient analysis also showed the direct and significant effects of grain protein percentage and medium direct effect of falling number on SDS sedimentation. This result can be used in wheat breeding programs.

Keywords: bread wheat, quality traits, correlation analysis

1. Introduction

The trait correlations are important in plant breeding, because of its reflection in dependence degree between two or more traits. Correlations between traits are depending of genetic and environmental factors (Falconer, 1981). Correlations themselves express only the degree of traits interrelationships, while path analysis provides analytically better survey of yield expression, as a resultant of its components. But it is not point to nature of that dependence. It is necessary to calculate path analysis of correlation coefficients, because this method enable quality and complete recognize ratio between investigation components. Since path-coefficient analysis was applied by Dewey and Lu (1959) on crested wheat grass, this technique has been followed extensively to facilitate selection in various crops. Existing correlation between components, expressed through correlation coefficients separate on direct and indirect influence by path method (Li, 1975; Penchev & Stoeva, 1989; Garcia Del Moral et al., 1991). Path coefficient analysis divides correlation coefficients into a measure of direct and indirect effects within a system of correlated traits. If there have been genetic relations among traits, selection for one trait would result in modification of another one, i.e. correlation response to selection would be obtained (Trifunovic, 1995). Correlation coefficient is helpful in determining main traits influencing grain protein content and grain yield for indirect selection criteria. However, it provides incomplete information regarding relative importance of direct and indirect effects on individual factors involved (Zecevic et al., 2004). Positive and significant correlations were observed among thousand kernel weight (TKW), kernel length (KL) and kernel width (KW), which suggested that selection for heavier kernels might lead to indirect selection for larger seeds (Ramya et al., 2010). In earlier studies, Dholakia et al. (2003) and Brescghello and Sorrels (2007) reported positive correlations among kernel weight, Huang et al. (2006) indicated that grain protein content (GPC) was highly correlated with flour protein content (FPC). Both GPC and FPC showed a positive correlation with SDS sedimentation volume (SV) and most mixograph parameters except mixing development time (MDT) and energy to peak (ETP). They also reported the strongest correlation ($r = 0.943$) between MDT and ETP. Negative correlations were found between grain yield and GPC ($r = -0.043$), but were not significant. Radovanovic et al.

(2002) reported that grain protein concentration was not significantly affected by HMW glutenin composition. Tayyar (2010) showed that grain yield was negatively correlated with gluten and positively correlated with hectoliter weight whereas there was no correlation with protein, gluten index and grain moisture. Jochen et al. (2011) reported that low and high phenotypic correlations between 1000-kernel weight and test weight ($r = 0.04$) and between protein content and sedimentation volume ($r = 0.60$) were exist. The higher SDS sedimentation volume causes more gluten strength. SDS sedimentation volume, were correlated with qualitative traits, including volume of bread, gluten strength and protein content. Therefore, SDS sedimentation volume is an appropriate tool for predicting the breadmaking properties in bread wheat (Campbell et al., 1987; Grama et al., 1987; Gupta et al., 1995). Shahin Nia et al. (2002) reported that positive significant correlation between protein percentage, SDS sedimentation test and other bread-making quality traits were exist. On the first and second steps of stepwise regression analysis, protein percentage was the most effective trait in explaining different qualitative trait variations. Path analysis also showed the direct and significant effects of protein percentage, Zeleny sedimentation volume, grain moisture content and flour water absorption percentage, and bread volume on SDS sedimentation.

The present study was initiated to investigate the interrelationship of some wheat traits and the type and extent of their contribution to seed quality of bread wheat. The information's so derived could be exploited in devising further breeding strategies and selection procedures to develop new varieties of wheat capable of high productivity.

2. Materials and Methods

2.1 Plant Materials and Experimental Design

This study was carried out in Research Field of Seed and Plant Improvement Institute, Karaj, Iran, during 2011-2012 cropping season. The materials consisted of Ninety-two bread wheat genotypes (including 82 cultivar and 10 promising breeding lines, Table 1), that either have been cultivated previously or are under cultivation at present in different regions of Iran and used widely in wheat production as well. An alpha lattice design with two replications were used, each plot contained 4 rows, 20 cm apart and 4 m in length.

2.2 Measurement of Kernel Quality Traits

Grain protein percentage and grain hardness were estimated by Near-Infrared-Reflectance (respectively method AACC 39-10 and method AACC 39-70A). The gluten content was determined by method AACC 38-12. The SDS sedimentation volume was determined by measuring the SDS sedimentation volume according to method AACC No, 56-70. The falling number was determined by method AACC No, 56-81. GW, GL and TKW of wheat genotypes were measured using a balance with an accuracy of 0.01gr. Analysis of variance, correlation among traits, stepwise multivariate regression and path analysis were performed using *alpha*, *SPSS* and *Path2 software*, respectively.

3. Results and Discussion

3.1 Analysis of Variance and Correlation Analysis

Analysis of variance showed significant differences for all traits, except for falling number (Table 2). The significant difference among genotypes for traits implies the presence of variation among genotypes. Correlations among all traits measured are summarized in Table 3. Thousand kernel weight (TKW) had significant positive correlation with grain length (GL) and grain width (GW) respectively ($r = 0.68^{**}$ and $r = 0.39^{**}$).

Table 1. Names of bread wheat genotypes used in the study

No	Name/Identity	Growth type	No	Name/Identity	Growth type
1	Karaj-1	Facultative	47	Morvarid	Spring
2	Karaj-2	Facultative	48	Gonbad	Spring
3	Karaj-3	Winter	49	Arvand	Spring
4	Azadi	Spring	50	Chenab	Spring
5	Ghods	Spring	51	Bayat	Spring
6	Mahdavi	Facultative	52	Falat	Spring
7	Niknejad	Spring	53	Heirmand	Spring
8	Marvdasht	Spring	54	Darab-2	Spring
9	Pishtaz	Spring	55	Atrak	Spring
10	Shiraz	Spring	56	Chamran	Spring
11	Sepahan	Spring	57	Star	Spring
12	Bahar	Spring	58	Dez	Spring
13	Parsi	Spring	59	Vee/Nac	Spring
14	Sivand	Spring	60	Line A	Spring
15	M-85-7	Spring	61	Aflak	Spring
16	WS-82-9	Spring	62	Baaz	Spring
17	Sirvan	Spring	63	Shahpasand	Winter
18	DN-11	Spring	64	Omid	Winter
19	Bezostaya	Winter	65	Roshan	Facultative/Spring
20	Navid	Facultative/Winter	66	Tabassi	Facultative
21	Alamout	Facultative/Winter	67	Sholleh	Spring
22	Alvand	Facultative	68	Sorkhtokhm	Spring
23	Zarin	Facultative	69	Adl	Facultative
24	MV-17	Winter	70	Sardari	Winter
25	Gaspard	Winter	71	Azar-2	Winter
26	Gascogne	Winter	72	Zagross	Spring
27	Soisson	Winter	73	Sabalan	Winter
28	Shahriar	Winter	74	Sp.Bc of Roshan	Spring
29	Tous	Winter	75	Wi. Bc of Roshan	Winter
30	Pishgam	Facultative	76	Cross of Shahi	Winter
31	Mihan	Winter	77	Maroon	Spring
32	Oroom	Facultative	78	Kavir	Spring
33	Zaree	Winter	79	Hamoon	Spring
34	Inia	Spring	80	Bam	Spring
35	Khazar-1	Spring	81	Akbari	Spring
36	Mughan-1	Spring	82	Sistan	Spring
37	Mughan-2	Spring	83	Arg	Spring
38	Mughan-3	Spring	84	UN-11	Winter
39	Golestan	Spring	85	Kohdasht	Spring
40	Alborz	Spring	86	Ohadi	Winter
41	Kaveh	Facultative	87	Rijav	Facultative
42	Rassoul	Spring	88	Rasad	Winter
43	Tajan	Spring	89	Karim	Spring
44	Shiroudi	Spring	90	Ch	Winter
45	Darya	Spring	91	Homa	Winter
46	Arta	Spring	92	Norstar	Winter

Table 2. Analysis of variance of traits

S. O. V	df	MS			
		Protein percentage	Hardness index	Gluten weight	SDS Sedimentation
Replication	1	4.11	33.62	744.98	5.44
Block (adjustment)	18	0.046	8.37	18.49	2.97
Treatment	99	0.41	16.20	15.18	39.09
Treatment (adjustment)	99	0.78 **	13.69 **	7.71 *	35.68 **
Residual	81	0.047	5.56	4.74	3.01
Total	199				

Table 2. Continued

	Grain length	Grain width	Thousand kernel weight	Falling number
	5.74	1.36	9.30	275356.10
	0.04	0.09	4.66	8281.92
	0.53	0.19	34.95	9898.16
	0.44 **	0.19 **	26.23 **	8407.60 ^{ns}
	0.07	0.08	3.12	6236.85

Table 3. Simple correlation coefficients matrix belonging to traits

Trait	1	2	3	4	5	6	7	8
1-Protein percentage	1							
2-Hardness index	0.36**	1						
3-Gluten weight	0.53**	0.14	1					
4-SDS sedimentation	0.22**	-0.08	0.10	1				
5-Grain length	0.18	0.07	0.21*	0.08	1			
6-Grain width	0.21**	0.05	0.19	0.08	0.26**	1		
7-Thousand kernel weight	0.33**	0.18	0.23*	-0.04	0.68**	0.39**	1	
8- Falling number	0.25**	0.12	0.34**	0.15	-0.04	0.17	0.17	1

These suggesting that heavier and larger kernels had a higher TKW. This result was in agreement with the works of Zecevic et al. (2004) and Ramya et al. (2010). Additionally our results were in agreement with Lee et al. (2006), who reported strong correlation ($r = 0.83$) between kernel weight and size. TKW, GL and GW had positive correlation with protein percentage, gluten weight, and falling number. Several researchers have also reported that kernel weight and size are important because of their relationships with milling quality, for example, an increase in flour yield resulted from an increase in kernel weight (Wiersema et al., 2001), or kernel size (Marshall et al., 1984; Berman et al., 1996).

However, the improvement of kernel weight and size alone has generally been found to have no benefits on grain yield. Protein percentage was significantly correlated with several kernel characteristics including: Hardness index, gluten weight, SDS sedimentation, TKW, GL, GW and falling number. These were agreement with results of Shahin Nia et al. (2002) that reported positive and significant relationship between protein percentage, SDS sedimentation test and other bread-making quality traits.

Gliadins and glutenins are major storage protein of wheat. These are the main component of gluten, which are primarily responsible for the viscoelasticity on dough and breadmaking properties (Branlard et al., 2001). In

general high grain protein content has been associated with good breadmaking quality. The wheat grain protein content is affected by some factors such as variety, location, crop year, temperature, rainfall, soil fertility etc. These are most important points for the producers as well as flour technologists, millers and bakers (Tayyar, 2010). Previous study also pointed out that the protein content of wheat was mainly dependent upon genotype (Stoddard, 1990). There were no undesirable relationships among other traits.

3.2 Stepwise Regression and Path Analysis

Using stepwise regression protein percentage and falling number were the most important component. These traits were the most effective trait in explaining different qualitative trait variations (Table 4), in the case of grain protein, these result also reported by Shahin Nia et al. (2002). Estimates of direct effect path coefficient and indirect effect path coefficient are presented in Table 5. Grain protein percentage had significant and positive, falling number had medium direct effect on SDS sedimentation. This indicated that with regard to constant other variables, an increase of these traits, seed quality traits has been improved. This result was in agreement with those reported by Shahin Nia et al. (2002). The results of this analysis indicates that, in breeding programs selecting the best genotypes for these traits lead to increase protein content and consequently improve the baking quality of wheat. Fowler et al. (1990) and Campbell et al. (1987) in previous studies have pointed to this subject.

Table 4. Stepwise regression for kernel traits

Dependent variable (DP)	No	Variable Entered	R Square		MS Regression	<i>a</i>	Regression coefficient
			Relative	Cumulative			
	1	Protein	0.51	0.51	90.54	28.24	3.86**
	2	Falling number	0.49	0.100	177.40	25.71	-0.016*

DP = SDS. Sedimentation.

Table 5. Direct (parenthesis) and indirect effect of two traits

	X ₁	X ₂	Total
X ₁	(0.102)	0.048	0.15
X ₂	0.023	(0.217*)	0.24
X ₁ = Falling number		X ₂ = Protein percentage	
Dependent variable: SDS, Sedimentation			

In Table 2, 3, 4 and 5, * and **: significant at 5%, 1% probability levels, respectively.

In Table 2 and 4: MS = Mean Square.

4. Conclusion

The present study depicted substantial variation among bread wheat genotypes for seed quality traits, which gives an opportunity to plant breeders to improve these traits. It is evident according to the results of this study, to evolve bread wheat genotypes with ultimate higher seed quality traits, attention should be focused selecting plant traits which have positive direct effect on seed quality traits.

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References

- AACC. (2000). Approved methods of American Association of Cereal Chemists, ST. Paul, Minnesota, USA.
- Berman, M., Bason, M. L., Ellison, R., Peden, G., & Wrigley, C. W. (1996). Image analysis of the whole grains to screen for flour-milling yield in wheat breeding. *Cereal Chem*, 73, 323-327.

- Branlard, G., Dardevet, M., Saccomano, R., Lagoutte, E., & Gourdon, J. (2001). Genetic diversity of wheat storage protein and bread wheat quality. *Euphytica*, 119, 59-67. <http://dx.doi.org/10.1023/A:1017586220359>
- Breseghele, F., & Sorrells, M. E. (2007). QTL analysis of kernel size and shape in two hexaploid wheat mapping populations. *Field Crop Res*, 101, 172-179. <http://dx.doi.org/10.1016/j.fcr.2006.11.008>
- Campbell, P., Wrigley, G. W., & Cressey, P. J. (1987). Statistical correlation between quality attributes and grain protein composition for 71 hexaploid wheat's used as breeding parent. *Cereal Chem*, 64, 293-299.
- Dewey, R. D., & Lu, K. H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron*, 52, 515-518.
- Dholakia, B. B., Ammiraju, J. S. S., Singh, H., Lagu, M. D, Roder, M. S., Rao, V. S., ... Weber, W. E. (2003). Molecular marker analysis of kernel size and shape in bread wheat. *Plant Breed*, 122, 392-395. <http://dx.doi.org/10.1046/j.1439-0523.2003.00896.x>
- Falconer, D. S. (1981). Introduction to quantitative genetics. Longman. London and New York.
- Garcia Del Moral, L. F., Ramos, J. M., Garcia Del Moral, M. B., & Jimenez-TE-Jada, M. P. (1991). Ontogenetic approach to grain production in spring barley based on path coefficient analysis. *Crop. Sci.*, 31, 1179-1185. <http://dx.doi.org/10.2135/cropsci1991.0011183X003100050021x>
- Grama, A., Cressey, P. J., & Lindly, T. (1987). Hexaploid wild emmer wheat derivatives grown under New Zealand conditions. I. Relationship between protein composition and quality parameters. *N. Z. J. Agric. Res*, 30, 35-43. <http://dx.doi.org/10.1080/00288233.1987.10430475>
- Gupta, R. B., Bekes, F., & Popineaut, Y. (1995). Biochemical basis of flour properties in bread wheat. *J. Cereal Sci*, 21, 103-116. [http://dx.doi.org/10.1016/0733-5210\(95\)90026-8](http://dx.doi.org/10.1016/0733-5210(95)90026-8)
- Huang, X. Q., Cloutier, S., Lycar, L., Radovanovic, N., Humphreys, D. G., Noll, J. S. D., ... Brown, P. D. (2006). Molecular detection of QTLs for agronomic and quality traits in a doubled haploid population derived from two Canadian wheat's (*Triticum aestivum* L.). *Theor Appl Genet*, 113, 753-766. <http://dx.doi.org/10.1007/s00122-006-0346-7>
- Jochen, C. R., Manje, G., Hans, P. M., Longin, V. K. C. F. H., Erhard, E., Reiner, B., ... Christof, P. T. W. (2011). Association mapping for quality traits in soft winter wheat. *Theor Appl Genet*, 22, 961-970.
- Lee, K-M., Shroyer, J. P, Herrman, T. J., & Lingenfelser, J. (2006). Blending hard white wheat to improve grain yield and end-use performances. *Crop Sci*, 46, 1124-1129. <http://dx.doi.org/10.2135/cropsci2005.07-0184>
- Li, C. C. (1975). *Path analysis - Example*. Box wood press. Pacific Grove. California.
- Marshall, D. R., Mares, D. J., Moss, H. J., & Ellison, F. W. (1984). Effects of grain shape and size on milling yields in wheat. Experimental studies. *Aust J Agric Res*, 37, 331-342. <http://dx.doi.org/10.1071/AR9860331>
- Penchev, E., & Stova, I. (1989). Mathematical model of wheat quality indices. *Bulgarian Plant Sci*, 26(3), 3-40
- Ramya, P., Chaubal, A., Kulkarni, K., Gupta, L., Kadoo, N., Dhaliwal, H. S., ... Gupta, V. (2010). QTL mapping of 1000-kernel weight, kernel length, and kernel width in bread wheat (*Triticum aestivum* L.). *J. Appl Genet*, 51, 421-429. <http://dx.doi.org/10.1007/BF03208872>
- Radovanovic, N., Cloutier, S., Brown, D., Humphreys, D. G., & Lukow O. M. (2002). Genetic variance for gluten strength contributed by high molecular weight glutenin proteins. *Cereal Chem*, 79, 843-849. <http://dx.doi.org/10.1094/CCHEM.2002.79.6.843>
- Shahin Nia, F., Rezaei, A., & Saedi, A. (2002). Variation and path coefficient analysis of bread making quality traits in breeding lines, cultivars and landrace varieties of wheat. *JWSS - Isfahan University of Technology*, 6, 77-89.
- Stoddard, F. L., & Marshal, D. R. (1990). Variability in grain protein in Australian hexaploid wheat's, *Aus. J. Agric. Res*, 41, 277-288. <http://dx.doi.org/10.1071/AR9900277>
- Tayyar, S. (2010). Variation in grain yield and quality of Romanian bread wheat varieties compared to local varieties in north-western Turkey. *Romanian Biotechnological Letters*, 15, 5189-5196.
- Trifunovic, B. (1995). Inheritance of prolificacy and genetic gain from phenotypic recurrent selection in the ZP Syn PI population of maize (*Zea mays* L.). *Arhiv za polj. Nauke*, 1-2, 3-40.

- Wiersma, J. J., Busch, R. H., Fulcher, G. G., & Hareland, G. (2001). Recurrent selection for kernel weight in spring wheat. *Crop Sci*, 41, 999-1005. <http://dx.doi.org/10.2135/cropsci2001.414999x>
- Zecevic, V., Knezevic, D., & Micanovic, D. (2004). Genetic correlation and path coefficient analysis of yield and quality component in wheat (*Triticum aestivum* L.). *Genetika*, 36, 13-21. <http://dx.doi.org/10.2298/GENSR0401013Z>

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